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OM nucleic - nucleic search, using sw model  
Run on: September 7, 2002, 22:32:16 ; Search time 1837.47 Seconds

(without alignments)  
1378.042 Million cell updates/sec

Title: US-09-719-017A-1  
Perfect score: 121  
Sequence: 1 gaatccctgttggacat...tatcttggaaataacttaca 121

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters:

3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% ,

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

1: gb:ba: \*  
2: gb:htg: \*  
3: gb:in: \*  
4: gb:on: \*  
5: gb:ov: \*  
6: gb:pat: \*  
7: gb:ph: \*  
8: gb:pl: \*  
9: gb:pr: \*  
10: gb:ro: \*  
11: gb:sts: \*  
12: gb:sy: \*  
13: gb:un: \*  
14: gb:vi: \*  
15: em:ba: \*  
16: em:fun: \*  
17: em:hum: \*  
18: em:in: \*  
19: em:mu: \*  
20: em:om: \*  
21: em:or: \*  
22: em:ov: \*  
23: em:pat: \*  
24: em:ph: \*  
25: em:pl: \*  
26: em:ro: \*  
27: em:sts: \*  
28: em:un: \*  
29: em:vi: \*  
30: em:htg:hum: \*  
31: em:htg:inv: \*  
32: em:htg:other: \*  
33: em:htg:inv: \*

### ALIGNMENTS

RESULT	1
AX008752	AX008752
LOCUS	Sequence 1 from Patent WO99664607.
DEFINITION	121 bp
ACCESSION	A008752
VERSION	AX008752.1
KEYWORDS	GI:9996243
SOURCE	Escherichia coli.
ORGANISM	Escherichia coli. Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
REFERENCE	1 (bases 1 to 121)
AUTHORS	Favre-Bulle,O., Guilton,C. and Pierrard,J.
TITLE	Industrial method for producing heterologous proteins in e.coli and strains useful for said method
JOURNAL	Patent: WO 9964607-A 1 16 DEC-1999;
FEATURES	FAVRE BULLE OLIVIER (FR); GUILTON CAROLE (FR); PIERRARD JEROME (FR); RHONE POULENC NUTRITION ANIMAL (FR)
SOURCES	Location/Qualifiers 1. .121 /organism="Escherichia coli" /db_xref="taxon:562"
BASE COUNT	37 a 27 c 23 g 34 t

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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## ORIGIN

	Db	121	A	121
RESULT	3			
Query Match	100.0%	Score 121;	DB 6;	Length 121;
Best Local Similarity	100.0%	Pred. No. 6.	3e-32;	
Matches	121;	Conservative	0;	Mismatches 0;
LOCUS	AX025996			
DEFINITION	Sequence 1 from Patent FR2787121.			
ACCESSION	AX025996			
VERSION	AX025996.1			
KEYWORDS				
SOURCE	Alcaligenes faecalis			
ORGANISM	Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;			
REFERENCE	1 (bases 1 to 1793)			
AUTHORS	Favre,B.O., Pierrard,J. and Batisse,D.N.			
JOURNAL	Patent: FR 2781121-A 1 16-JUN-2000;			
FEATURES	AVVENTIS CROPSCIENCE (FR)			
source	Location/Qualifiers			
	1. 1793			
	/organism="Alcaligenes faecalis"			
	/db_xref="taxon:511"			
CDS	123 . 1793			
	/note="unnamed protein product"			
	/codon_start=1			
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	/protein_id="CAC09060.1"			
	/db_xref="GI:10187455"			
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	SRSGSGSLVYLGQLCLDDKGQMLWSRKLPVHVERVFGGGYARQLPSLYSQHAAHLSAKVMAASQIYSEGQ			
	LCCWEHLSPLSKYALYSQHEAHITAWPERSLYEQAHLSAKVMAASQIYSEGQ			
	FTIAASSVVIQETDMLKEVGENHNSLKVGGGSMIFAPDQRTLAPYLPHDAEGLIA			
	DLNMEELAFAKAINDVNGHTSKPEATRLVLDLGHREPMTRVHSKSYVQEAEPEPHQS			
BASE COUNT	412	a	527	c 478 g 376 t
ORIGIN				
RESULT	4			
Query Match	100.0%	Score 121;	DB 6;	Length 1793;
Best Local Similarity	100.0%	Pred. No. 9.	9e-32;	
Matches	121;	Conservative	0;	Mismatches 0;
LOCUS	A06104			
DEFINITION	Insertion fragment to produce pfc80.			
ACCESSION	A06104			
VERSION	A06104.1			
KEYWORDS				
SOURCE	synthetic construct.			
ORGANISM	synthetic construct.			
REFERENCE	artificial sequence.			
	1 (bases 1 to 118)			
AUTHORS				
TITLE	NEW DERIVATIVES OF HUMAN/BOVINE BASIC FIBROBLAST GROWTH FACTOR			
JOURNAL	Patent: WO 9002800-A 10 22-MAR-1990;			
FEATURES	Location/Qualifiers			
source	1. .118			
	/organism="synthetic construct"			



FEATURES	source	FT	Key	CC	hypothetical; No;
BASE COUNT	28 a	/db_xref="taxon:4202"	PR	CC	*source: cell_line=pN6;
ORIGIN	22 c	16 g	PI	CC	Location/Qualifiers
Query Match	36.0%; Score 43.6; DB 6; Length 90;	FT	TAIKI NINOMIYA, TETSUYA MIWA, MINAO ASANO, NAMI NAKAMURA, PI	FH	-35-signal
Best Local Similarity	92.0%; Pred. No. 0.00011; Mismatches 0;	FT	TSUNERI NIO	FT	-10-signal
Matches 46;	Conservative 0; Mismatches 0;	FT	PC	FT	Location/Qualifiers
QY	2 aatccctgttgcataattatcatcgacttagttacttagtacacgctt 51	FT	C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10, PC	PR	1. .90
Db	9 ATTCCCCCTGTGACATAATTATCATCGAACTAGTTACTAGTACGCCAGTT 58	FT	C12N9/48//A23L1/238, PC	PR	/organism="unidentified plasmid"
RESULT 9		FT	C12N15/00,C12N5/00	CC	
LOCUS	AR172799	FT	Key	CC	promoter
DEFINITION	Sequence 3 from Patent US 6303359.	FT	Location/Qualifiers	CC	Location/Qualifiers
ACCESSION	AR172799	FT	0	CC	0 .357
VERSION	AR172799.1	FT	1.	CC	1. .357
KEYWORDS		FT	/organism="synthetic construct"	CC	
SOURCE	Unknown.	FT	/db_xref="taxon:32630"	CC	
ORGANISM	Unclassified.	FT	95 a	CC	90 c
REFERENCE	1. (bases 1 to 357)	FT	82 g	CC	90 t
AUTHORS	Ninomiya,D., Miwa,T., Asano,M., Nakamura,N. and Nio,N.	FT			
TITLE	DNA molecule encoding new aminopeptidase, and method of producing	FT			
FEATURES	the aminopeptidase	FT			
JOURNAL	Patent: US 6303359-A 3 16-OCT-2001;	FT			
SOURCE	1. .357	FT			
BASE COUNT	95 a	FT			
ORIGIN	90 c	FT			
Query Match	357 bp	FT			
Best Local Similarity	92.0%; Pred. No. 0.00015; Mismatches 0;	FT			
Matches 46;	Conservative 0; Mismatches 0;	FT			
QY	2 aatccctgttgcataattatcatcgacttagttacttagtacacgctt 51	FT			
Db	271 ATTCCCCCTGTGACATAATTATCATCGAACTAGTTACTAGTACGCCAGTT 320	FT			
RESULT 11		FT			
LOCUS	E31303	FT			
DEFINITION	process for producing novel microbial transglutaminase.	FT			
ACCESSION	E31303	FT			
VERSION	E31303.1	FT			
KEYWORDS	JP 1999075876-A/2.	FT			
SOURCE	unidentified.	FT			
ORGANISM	unclassified.	FT			
REFERENCE	1. (bases 1 to 1519)	FT			
AUTHORS	Keiichi,Y.N,N and Miwa,K.S.	FT			
TITLE	process for producing novel microbial transglutaminase	FT			
JOURNAL	Patent: JP 1999075876-A 2 23-MAR-1999;	FT			
COMMENT	AJINOMOTO CO INC	FT			
OS	Unidentified	FT			
PN	JP 1999075876-A/2	FT			
PD	23-MAR-1999	FT			
PR	29-JUN-1998	FT			
PI	KEIICHI YOKOYAMA, NAMI NAKAMURA, TETSUYA MIWA, KATSUYA SEGURO	FT			
C12N15/09,C12N1/21,C12N9/10//(C12N1/21,C12R1:19), (C12N9/10, PC	FT				
C12R1:19),	FT				
PC	C12N15/00	FT			
CC	Strandedness: Double;	FT			
KEY	Topology: Linear;	FT			
FEATURES	Location/Qualifiers	FT			
SOURCE	87 .1082.	FT			
BASE COUNT	355 a	FT			
ORIGIN	350 c	FT			
Query Match	35.7%; Score 43.2; DB 6; Length 1519;	FT			
Best Local Similarity	93.8%; Pred. No. 0.00026; Mismatches 3;	FT			
Matches 45;	Conservative 0; Mismatches 3;	FT			
QY	4 ttccctgttgcataattatcatcgacttagttacttagtacacgctt 51	FT			
Db	2 TCCCGTGTGACACATTATCATCGAACTAGTTACTAGTACGCCAGTT 49	FT			
RESULT 10		FT			
LOCUS	BD003394	FT			
DEFINITION	357 bp DNA linear	FT			
amino peptidase and process for producing the	PAT 31-JAN-2002	FT			
ACCESSION	BD003394	FT			
VERSION	BD003394.1	FT			
KEYWORDS	BD003394.1 GI:18623499	FT			
SOURCE	JP 200325090-A/2.	FT			
ORGANISM	synthetic construct.	FT			
REFERENCE	1. (bases 1 to 357)	FT			
AUTHORS	Ninomiya,T., Miwa,T., Asano,M., Nakamura,N. and Nio,T.	FT			
TITLE	DNA encoding novel amino peptidase and process for producing the	FT			
ACCESSION	BD003394	FT			
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ACCESSION	BD003394	FT			
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KEYWORDS	BD003394.1	FT			
SOURCE	JP 200325090-A/2.	FT			
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REFERENCE	1. (bases 1 to 357)	FT			
AUTHORS	Ninomiya,T., Miwa,T., Asano,M., Nakamura,N. and Nio,T.	FT			
TITLE	DNA encoding novel amino peptidase and process for producing the	FT			
ACCESSION	BD003394	FT			
VERSION	BD003394.1 GI:18623499	FT			
KEYWORDS	BD003394.1	FT			
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AUTHORS	Ninomiya,T., Miwa,T., Asano,M., Nakamura,N. and Nio,T.	FT			
TITLE	DNA encoding novel amino peptidase and process for producing the	FT			
ACCESSION	BD003394	FT			
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ACCESSION	BD003394	FT			
VERSION	BD003394.1 GI:18623499	FT			
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SOURCE	JP 200325090-A/2.	FT			
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REFERENCE	1. (bases 1 to 357)	FT			
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TITLE	DNA encoding novel amino peptidase and process for producing the	FT			
ACCESSION	BD003394	FT			
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SOURCE	JP 200325090-A 2 28-NOV-2000;	FT			
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AUTHORS	Ninomiya,T., Miwa,T., Asano,M., Nakamura,N. and Nio,T.	FT			
TITLE	DNA encoding novel amino peptidase and process for producing the	FT			
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VERSION	BD003394.1 GI:18623499	FT			
KEYWORDS	BD003394.1	FT			
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REFERENCE	1. (bases 1 to 357)	FT			
AUTHORS	Ninomiya,T., Miwa,T., Asano,M., Nakamura,N. and Nio,T.	FT			
TITLE	DNA encoding novel amino peptidase and process for producing the	FT			
ACCESSION</					

RESULT	12	Db	7	CCCTGTTGACATTATCATCGAAGCTAGTTAAGTACCCAG	49
ECOTRPPQ		RESULT	14		
LOCUS	ECOTRPPRO	DEFINITION	E00405		
DEFINITION	E. coli trp promoter region.	DEFINITION	E00405	DNA coding for trp promoter.	
ACCESSION	K01192	ACCESSION	E00405		
KEYWORDS	mutational analysis; promoter region; trp operon.	KEYWORDS	E00405.1	GI:2168668	
SOURCE	E. coli DNA	SOURCE	JP 198510881-A/1.		
ORGANISM	Escherichia coli	ORGANISM	unidentified Plasmid.		
REFERENCE	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.	REFERENCE	unidentified Plasmid.		
AUTHORS	1 (bases 1 to 62)	AUTHORS	plasmids.		
TITLE	Russell,D.R. and Bennett,G.N.	TITLE	1 (bases 1 to 63)		
JOURNAL	Construction and analysis of in vivo activity of E. coli promoter hybrids and promoter mutants that alter the -35 to -10 spacing	JOURNAL	Nakagawa,Y., Uno,S., Nagai,M. and Arimura,H.		
MEDLINE	Gene 20, 231-243 (1982)	MEDLINE	Patent: JP 1995160887-A 1 22-AUG-1985;		
COMMENT		COMMENT	GREEN CROSS CORP:THE		
	[1] examines the efficiency of gene expression in E. coli if the distance between the -35 and -10 regions is increased and also when the -35 region from one and the -10 region from another gene are recombined to form a hybrid promoter region. In every case it was found that the spacing between these two regions was of prime importance and can not be greater than 18 bp in a functional promoter.		OS plasmid		
FEATURES	Location/Qualifiers	FEATURES	PN JP 1985160887-A/1		
source	1. .62	source	PD 22-AUG-1985		
Qy	/organism="Escherichia coli"	Qy	PF 02-FEB-1984 JP 1984018133		
Db	/db_xref="taxon:562"	Db	PI NAKAGAWA YUKIMITSU, UNO SHUSEI, NAGAI MASANORI, PI ARIMURA HIROMI		
	20. .25		PC C12N15/00//C07H21/04;		
	-10_signal 43. .48		CC strandedness: Single;		
	20. .25		CC topology: Linear;		
	BASE COUNT 17 a 19 c		CC hypothetical: No;		
	ORIGIN 27.7 min on K12 map.		Key FH		
			Location/Qualifiers		
			FT -35_signal 5. .10		
			FT -10_signal 28. .33		
			FT RBS 57. .60.		
		FEATURES	1. .63		
		source	/organism="unidentified plasmid"		
			/db_xref="taxon:45202"		
		BASE COUNT	22 a 13 c 11 g		
		ORIGIN	17 t		
RESULT	13	Query Match	35.5%	Score 43;	DB 1; Length 62;
SYNMDVA		Best Local Similarity	100.0%	Pred. No.	0.00018; Mismatches
LOCUS	SYNMDVA	0; Indels	0;	0;	0; Gaps
DEFINITION	Synthetic plasmid pSL1 DNA fragment.	FEATURES			
ACCESSION	M31473	source			
VERSION	M31473.1	BASE COUNT			
KEYWORDS		ORIGIN			
SOURCE	Synthetic DNA, clone pSL1.	Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
ORGANISM	unidentified cloning vector.	Db	48		
VERSION		Query Match	35.4%	Score 42.8;	DB 6; Length 63;
		Best Local Similarity	95.7%	Pred. No.	0.00021; Mismatches
		Matches	44;	0;	0; Indels
		FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
RESULT	15	Query Match	35.4%	Score 42.8;	DB 6; Length 63;
AJ2512		Best Local Similarity	95.7%	Pred. No.	0.00021; Mismatches
DEFINITION	trp promoter and transcriptional start site.	Matches	44;	0;	0; Indels
ACCESSION	A12512	FEATURES			
VERSION	A12512.1	source			
KEYWORDS		BASE COUNT			
SOURCE		ORIGIN			
ORGANISM	synthetic construct.	Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
FEATURES	synthetic construct.	Db	46		
source	artificial sequence.	Query Match	35.4%	Score 42.8;	DB 6; Length 63;
1. .269	1 (bases 1 to 269)	Best Local Similarity	95.7%	Pred. No.	0.00021; Mismatches
/organism="unidentified cloning vector"	Lafaille, S. E., Kramer, F. R. and Mills, D. R.	Matches	44;	0;	0; Indels
/db_xref="taxon:45196"	Comparison of pausing during transcription and replication	FEATURES			
BASE COUNT	49 a 92 c 83 g 45 t	source			
ORIGIN		BASE COUNT			
Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg	ORIGIN			
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42.4;	DB 6; Length 44;
		Best Local Similarity	100.0%	Pred. No.	0.00023; Mismatches
	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES			
		source			
		BASE COUNT			
		ORIGIN			
		Qy	6 ccctgttggacattaaatcatcgaaacttagttactgttacgcgg		
		Query Match	35.0%	Score 42	

Best Local Similarity 97.7%; Pred. No. 0 00027; Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 8 ctgttgacaatataatcatcgacttagttactgttgcgtt 51  
Db 1 CTGTTGACAATATAATCATCGACTTAGTTACTGTACGAAGCTT 44

Search completed: September 8, 2002, 00:37:47  
Job time: 7531 sec